SEQUENCE LISTING

<110> SHEPPARD. PAUL O.
      GILBERT. THERESA

<120> SECRETED PROTEIN. ZSIG47

<130> 00-32C1

<150> 60/206.179
<151> 2000-05-22

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aca gcc gcg cag cgg agg tgt tcg ttg ccg ccg tgg ctg ccg ctg ggg      104
Thr Ala Ala Gln Arg Arg Cys Ser Leu Pro Pro Trp Leu Pro Leu Gly
             10              15                  20

ctg ctg ctg tgg tcg ggg ctg gcc ctg ggc gcg ctc ccc ttc ggc agc      152
Leu Leu Leu Trp Ser Gly Leu Ala Leu Gly Ala Leu Pro Phe Gly Ser
             25              30                  35

agt ccg cac agg gtc ttc cac gac ctc ctg tcg gag cag cag ttg ctg      200
Ser Pro His Arg Val Phe His Asp Leu Leu Ser Glu Gln Gln Leu Leu
         40              45                  50
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gag gtg gag gac ttg tcc ctg tcc ctc ctg cag ggt gga ggg ctg ggg        248
Glu Val Glu Asp Leu Ser Leu Ser Leu Leu Gln Gly Gly Gly Leu Gly
     55                      60                  65

cct ctg tcg ctg ccc ccg gac ctg ccg gat ctg gat cct gag tgc cgg        296
Pro Leu Ser Leu Pro Pro Asp Leu Pro Asp Leu Asp Pro Glu Cys Arg
 70                      75                  80                  85

gag ctc ctg ctg gac ttc gcc aac agc agc gca gag ctg aca ggg tgt        344
Glu Leu Leu Leu Asp Phe Ala Asn Ser Ser Ala Glu Leu Thr Gly Cys
                     90                  95                  100

ctg gtg cgc agc gcc cgg ccc gtg cgc ctc tgt cag acc tgc tac ccc        392
Leu Val Arg Ser Ala Arg Pro Val Arg Leu Cys Gln Thr Cys Tyr Pro
                 105                 110                 115

ctc ttc caa cag gtc gtc agc aag atg gac aac atc agc cga gcc gcg        440
Leu Phe Gln Gln Val Val Ser Lys Met Asp Asn Ile Ser Arg Ala Ala
                 120                 125                 130

ggg aat act tca gag agt cag agt tgt gcc aga agt ctc tta atg gca        488
Gly Asn Thr Ser Glu Ser Gln Ser Cys Ala Arg Ser Leu Leu Met Ala
             135                 140                 145

gat aga atg caa ata gtt gtg att ctc tca gaa ttt ttt aat acc aca        536
Asp Arg Met Gln Ile Val Val Ile Leu Ser Glu Phe Phe Asn Thr Thr
150                 155                 160                 165

tgg cag gag gca aat tgt gca aat tgt tta aca aac aac agt gaa gaa        584
Trp Gln Glu Ala Asn Cys Ala Asn Cys Leu Thr Asn Asn Ser Glu Glu
                 170                 175                 180

tta tca aac agc aca gta tat ttc ctt aat cta ttt aat cac acc ctg        632
Leu Ser Asn Ser Thr Val Tyr Phe Leu Asn Leu Phe Asn His Thr Leu
             185                 190                 195

acc tgc ttt gaa cat aac ctt cag ggg aat gca cat agt ctt tta cag        680
Thr Cys Phe Glu His Asn Leu Gln Gly Asn Ala His Ser Leu Leu Gln
             200                 205                 210

aca aaa aat tat tca gaa gta tgc aaa aac tgc cgt gaa gca tac aaa        728
Thr Lys Asn Tyr Ser Glu Val Cys Lys Asn Cys Arg Glu Ala Tyr Lys
     215                 220                 225
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act ctg agt agt ctg tac agt gaa atg caa aaa atg aat gaa ctt gag        776
Thr Leu Ser Ser Leu Tyr Ser Glu Met Gln Lys Met Asn Glu Leu Glu
230             235             240             245

aat aag gct gaa cct gga aca cat tta tgc att gat gtg gaa gat gca        824
Asn Lys Ala Glu Pro Gly Thr His Leu Cys Ile Asp Val Glu Asp Ala
            250             255             260

atg aac atc act cga aaa cta tgg agt cga act ttc aac tgt tca gtc        872
Met Asn Ile Thr Arg Lys Leu Trp Ser Arg Thr Phe Asn Cys Ser Val
            265             270             275

cct tgc agt gac aca gtg cct gta att gct gtt tct gtg ttc att ctc        920
Pro Cys Ser Asp Thr Val Pro Val Ile Ala Val Ser Val Phe Ile Leu
            280             285             290

ttt cta cct gtt gtc ttc tac ctt agt agc ttt ctt cac tca gag caa        968
Phe Leu Pro Val Val Phe Tyr Leu Ser Ser Phe Leu His Ser Glu Gln
        295             300             305

aag aaa cgc aaa ctc att ctg ccc aaa cgt ctc aag tcc agt acc agt       1016
Lys Lys Arg Lys Leu Ile Leu Pro Lys Arg Leu Lys Ser Ser Thr Ser
310             315             320             325

ttt gca aat att cag gaa aat tca aac tga gacctacaaa atggagaatt         1066
Phe Ala Asn Ile Gln Glu Asn Ser Asn *
            330

gacatatcac gtgaatgaat ggtggaagac acaacttggt ttcagaaaga agataaactg   1126
tgatttgaca agtcaagctc ttaagaaata caaggacttc agatccattt ttaaataaga   1186
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ttgcagtatt attgttatat atatagttaa tatgttgtac atcacaataa tatataattc   1546
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atcaaatgta gcattatcac actgtatttta aattgtcatt ttttaaagga atattttctt   1906
cttaagatat atagaggatt ttggagaaga gagacaggag gggtaaaacc agcttaaggt   1966
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tcagcgagca gaaagggacc tgagaggatg ctcactgtaa gactgttgga cagtggtgtg   2026
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cttattgttt ctaaattatt tcaatcagat gaaagtgata cgattgaaat gaaatcacat   2146
agttcgtgct cagaaattct attttggtat gtttgtatta gcctttagaa aaaacactcc   2206
gtttcagaat tgttcacagt tttatttctt aggttttttag agttcaggat ttcatttatt   2266
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taaaatgctc tatagggaga caaagtgttt cttttttctt ttatgtttac tgtttatgtg   2446
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ggaacttagc actgtcttga tttgaagcat atgattgaga gccatttgaa gcaatcttca   2626
ttaatgcaga taaaacaagt ttacatgtgc agagttagaa aatgacatgt tcaattctgt   2686
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Leu Pro Phe Gly Ser Ser Pro His Arg Val Phe His Asp Leu Leu Ser
            35                  40                  45
Glu Gln Gln Leu Leu Glu Val Glu Asp Leu Ser Leu Ser Leu Leu Gln
        50                  55                  60
Gly Gly Gly Leu Gly Pro Leu Ser Leu Pro Pro Asp Leu Pro Asp Leu
65                  70                  75                  80
Asp Pro Glu Cys Arg Glu Leu Leu Leu Asp Phe Ala Asn Ser Ser Ala
                85                  90                  95
Glu Leu Thr Gly Cys Leu Val Arg Ser Ala Arg Pro Val Arg Leu Cys
            100                 105                 110
Gln Thr Cys Tyr Pro Leu Phe Gln Gln Val Val Ser Lys Met Asp Asn
            115                 120                 125
Ile Ser Arg Ala Ala Gly Asn Thr Ser Glu Ser Gln Ser Cys Ala Arg
        130                 135                 140
Ser Leu Leu Met Ala Asp Arg Met Gln Ile Val Val Ile Leu Ser Glu
145                 150                 155                 160
Phe Phe Asn Thr Thr Trp Gln Glu Ala Asn Cys Ala Asn Cys Leu Thr
                165                 170                 175
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Asn Asn Ser Glu Glu Leu Ser Asn Ser Thr Val Tyr Phe Leu Asn Leu
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Phe Asn His Thr Leu Thr Cys Phe Glu His Asn Leu Gln Gly Asn Ala
          195   200   205
His Ser Leu Leu Gln Thr Lys Asn Tyr Ser Glu Val Cys Lys Asn Cys
          210   215   220
Arg Glu Ala Tyr Lys Thr Leu Ser Ser Leu Tyr Ser Glu Met Gln Lys
225   230   235   240
Met Asn Glu Leu Glu Asn Lys Ala Glu Pro Gly Thr His Leu Cys Ile
          245   250   255
Asp Val Glu Asp Ala Met Asn Ile Thr Arg Lys Leu Trp Ser Arg Thr
          260   265   270
Phe Asn Cys Ser Val Pro Cys Ser Asp Thr Val Pro Val Ile Ala Val
          275   280   285
Ser Val Phe Ile Leu Phe Leu Pro Val Val Phe Tyr Leu Ser Ser Phe
290   295   300
Leu His Ser Glu Gln Lys Lys Arg Lys Leu Ile Leu Pro Lys Arg Leu
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Lys Ser Ser Thr Ser Phe Ala Asn Ile Gln Glu Asn Ser Asn
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mgngtnttyc aygayytnyt nwsngarcar carytnytng argtngarga yytnwsnytn   180
wsnytnytnc arggnggngg nytnggnccn ytnwsnytnc cnccngayyt nccngayytn   240
gayccngart gymgngaryt nytnytngay ttygcnaayw snwsngcnga rytnacnggn   300

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tgyytngtnm gnwsngcnmg nccngtnmgn ytntgycara cntgytaycc nytnttycar      360
cargtngtnw snaaratgga yaayathwsn mgngcngcng gnaayacnws ngarwsncar      420
wsntgygcnm gnwsnytnyt natggcngay mgnatgcara thgtngtnat hytnwsngar      480
ttyttyaaya cnacntggca rgargcnaay tgygcnaayt gyytnacnaa yaaywsngar      540
garytnwsna aywsnacngt ntayttyytn aayytnttya aycayacnyt nacntgytty      600
garcayaayy tncarggnaa ygcncaywsn ytnytncara cnaaraayta ywsngargtn      660
tgyaaraayt gymgngargc ntayaaracn ytnwsnwsny tntaywsnga ratgcaraar      720
atgaaygary tngaraayaa rgcngarccn ggnacncayy tntgyathga ygtngargay      780
gcnatgaaya thacnmgnaa rytntggwsn mgnacnttya aytgywsngt nccntgywsn      840
gayacngtnc cngtnathgc ngtnwsngtn ttyathytnt tyytnccngt ngtnttytay      900
ytnwsnwsnt tyytncayws ngarcaraar aarmgnaary tnathytncc naarmgnytn      960
aarwsnwsna cnwsnttygc naayathcar garaaywsna ay                        1002
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